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NEWS 1		Web Page URLs for STN Seminar Schedule - N. America
NEWS 2	Sep 17	IMSworld Pharmaceutical Company Directory name change to PHARMASEARCH
NEWS 3	Oct 09	Korean abstracts now included in Derwent World Patents Index
NEWS 4	Oct 09	Number of Derwent World Patents Index updates increased
NEWS 5	Oct 15	Calculated properties now in the REGISTRY/ZREGISTRY File
NEWS 6	Oct 22	Over 1 million reactions added to CASREACT
NEWS 7	Oct 22	DGENE GETSIM has been improved
NEWS 8	Oct 29	AAASD no longer available
NEWS 9	Nov 19	New Search Capabilities USPATFULL and USPAT2
NEWS 10	Nov 19	TOXCENTER(SM) - new toxicology file now available on STN
NEWS 11	Nov 29	COPPERLIT now available on STN
NEWS 12	Nov 29	DWPI revisions to NTIS and US Provisional Numbers
NEWS 13	Nov 30	Files VETU and VETB to have open access
NEWS 14	Dec 10	WPINDEX/WPIDS/WPIX New and Revised Manual Codes for 2002
NEWS 15	Dec 10	DGENE BLAST Homology Search
NEWS 16	Dec 17	WELDASEARCH now available on STN
NEWS 17	Dec 17	STANDARDS now available on STN
NEWS 18	Dec 17	New fields for DPCI
NEWS 19	Dec 19	CAS Roles modified
NEWS 20	Dec 19	1907-1946 data and page images added to CA and CAplus
NEWS 21	Jan 25	BLAST(R) searching in REGISTRY available in STN on the Web
NEWS 22	Jan 25	Searching with the P indicator for Preparations
NEWS 23	Jan 29	FSTA has been reloaded and moves to weekly updates
NEWS 24	Feb 01	DKILIT now produced by FIZ Karlsruhe and has a new update frequency
NEWS 25	Feb 19	Access via Tymnet and SprintNet Eliminated Effective 3/31/02
NEWS 26	Mar 08	Gene Names now available in BIOSIS
NEWS 27	Mar 22	TOXLIT no longer available
NEWS 28	Mar 22	TRCTHERMO no longer available

NEWS EXPRESS	February 1 CURRENT WINDOWS VERSION IS V6.0d, CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND V6.0Ja(JP), AND CURRENT DISCOVER FILE IS DATED 05 FEBRUARY 2002
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FILE 'HOME' ENTERED AT 11:21:04 ON 25 MAR 2002

=> file, medline, caplus, scisearch, biosis, enbase
FILE, IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> file medline, caplus, scisearch, biosis, enbase
'ENBASE' IS NOT A VALID FILE NAME
Enter "HELP FILE NAMES" at an arrow prompt (=>) for a list of files
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specify a corrected file name or you can enter "IGNORE" to continue
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ENTER A FILE NAME OR (IGNORE):file medline, caplus, scisearch, biosis, embase
'FILE' IS NOT A VALID FILE NAME
Enter "HELP FILE NAMES" at an arrow prompt (=>) for a list of files
that are available.  If you have requested multiple files, you can
specify a corrected file name or you can enter "IGNORE" to continue
accessing the remaining file names entered.
ENTER A FILE NAME OR (IGNORE):file medline, caplus, scisearch, biosis, embase
'FILE' IS NOT A VALID FILE NAME
Enter "HELP FILE NAMES" at an arrow prompt (=>) for a list of files
that are available.  If you have requested multiple files, you can
specify a corrected file name or you can enter "IGNORE" to continue
accessing the remaining file names entered.
ENTER A FILE NAME OR (IGNORE):end

=> file medline, caplus, scisearch, biosis, embase
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                                              ENTRY    SESSION
FULL ESTIMATED COST                            1.20       1.20

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=> s pentapeptide and concatemer
=> s penta p peptide
L1             0 PENTA P PEPTIDE

=> s pentapeptide
L2         14693 PENTAPEPTIDE

=> s l2 and seq id 16
L3             0 L2 AND SEQ ID 16
```

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=> s l2 and catamer
=> s l2 and recombination
L4          25 L2 AND RECOMBINATION

=> s l4 and cell with culture
   4 FILES SEARCHED...
L5           4 L4 AND CELL WITH CULTURE

=> dl5 1-4 ibib abs
DL5 IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> d l5 1-4 ibib abs

L5   ANSWER 1 OF 4     MEDLINE
ACCESSION NUMBER:    92391103     MEDLINE
DOCUMENT NUMBER:     92391103   PubMed ID: 1381539
TITLE:               Biologically selected recombinants between feline leukemia
                     virus (FeLV) subgroup A and an endogenous FeLV element.
AUTHOR:              Sheets R L; Pandey R; Klement V; Grant C K; Roy-Burman P
CORPORATE SOURCE:    Department of Pathology, University of Southern California
                     School of Medicine, Los Angeles 90033.
CONTRACT NUMBER:     CA51485 (NCI)
SOURCE:              VIROLOGY, (1992 Oct) 190 (2) 849-55.
                     Journal code: XEA; 0110674. ISSN: 0042-6822.
PUB. COUNTRY:        United States
                     Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
ENTRY MONTH:         199210
ENTRY DATE:          Entered STN: 19921023
                     Last Updated on STN: 19970203
                     Entered Medline: 19921008
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AB In efforts to elucidate the proximal leukemogens that might be produced during a feline leukemia virus (FeLV) infection of cats, homologous **recombinations** between molecularly cloned exogenous and endogenous FeLV proviruses of known sequences were examined in **cell cultures** in vitro. A plasmid containing an infectious member of the most commonly occurring FeLV subgroup (FeLV subgroup A or FeLV-A) was coexpressed with noninfectious constructs containing the envelope (env) gene of an endogenously inherited FeLV-like feline genomic element in transfected feline fibroblasts. The viruses generated were selected for their ability to propagate in human cells which are resistant to infection by the parental ecotropic FeLV-A or the noninfectious endogenous constructs. An analysis of the recombinants thus derived identified a limited number of sites in the env gene which were preferentially utilized in the generation of recombinant FeLVs under the selection conditions used. These sites were clustered in the surface glycoprotein (SU) moiety of the env gene, and it appeared that most, but not all, of the SU gene product of FeLV-A, beginning from the N-terminus, can be replaced by sequences from an endogenous element, still allowing the virus to be biologically viable. In fact, these substitutions in the env gene expanded infectivity of the parental FeLV-A from ecotropic to polytropic cell tropism. Additionally, substitutions in the SU region yielded many recombinants in which a primary neutralizing **pentapeptide** epitope of FeLV-A was altered because of its variance in the endogenous element. In several of the recombinants, this sequence was also found to be frequently mutated. Consistent with the changes identified in this antibody-binding domain, the recombinant viruses were only weakly inhibited by a monoclonal antibody directed against this epitope, while

FeLV-A was highly sensitive to neutralization.

L5 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1992:631321 CAPLUS
DOCUMENT NUMBER: 117:231321
TITLE: Biologically selected recombinants between feline leukemia virus (FeLV) subgroup A and an endogenous FeLV element
AUTHOR(S): Sheets, Rebecca Lynn; Pandey, Rakesh; Klement, VAclav; Grant, Chris K.; Roy-Burman, Pradip
CORPORATE SOURCE: Sch. Med., Univ. Southern California, Los Angeles, CA, 90033, USA
SOURCE: Virology (1992), 190(2), 849-55
CODEN: VIRLAX; ISSN: 0042-6822
DOCUMENT TYPE: Journal
LANGUAGE: English
AB In efforts to elucidate the proximal leukemogens that might be produced during a feline leukemia virus (FeLV) infection of cats, homologous **recombinations** between molecularly cloned exogenous and endogenous FeLV proviruses of known sequences were examd. in **cell cultures** in vitro. A plasmid contg. an infectious member of the most commonly occurring FeLV subgroup (FeLV subgroup A or FeLV-A) was co-expressed with non-infectious constructs contg. the envelope (env) gene of an endogenously inherited FeLV-like feline genomic element in transfected feline fibroblasts. The viruses generated were selected for their ability to propagate in human cells which are resistant to infection by the parental ecotropic FeLV-A or the noninfectious endogenous constructs. An anal. of the recombinants thus derived identified a limited no. of sites in the env gene which were preferentially utilized in the generation of recombinant FeLVs under the selection conditions used. These sites were clustered in the surface glycoprotein (SU) moiety of the env gene, and it appeared that most, but not all, of the SU gene product of FeLV-A, beginning from the N-terminus, can be replaced by sequences from an endogenous element, still allowing the virus to be biol. viable. In fact, these substitutions in the env gene expanded infectivity of the parental FeLV-A from ecotropic to polytropic cell tropism. Addnl., substitutions in the SU region yielded many recombinants in which a primary neutralizing **pentapeptide** epitope of FeLV-A was altered because of its variance in the endogenous element. In several of the recombinants, this sequence was also found to be frequently mutated. Consistent with the changes identified in this antibody-binding domain, the recombinant viruses were only weakly inhibited by a monoclonal antibody directed against this epitope, while FeLV-A was highly sensitive to neutralization.

L5 ANSWER 3 OF 4 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1992:503767 BIOSIS
DOCUMENT NUMBER: BA94:122292
TITLE: BIOLOGICALLY SELECTED RECOMBINANTS BETWEEN FELINE LEUKEMIA VIRUS FELV SUBGROUP A AND AN ENDOGENOUS FELV ELEMENT.
AUTHOR(S): SHEETS R L; PANDEY R; KLEMENT V; GRANT C K; ROY-BURMAN P
CORPORATE SOURCE: DEP. PATHOL., UNIV. SOUTHERN CALIF. SCH. MED., LOS ANGELES, CALIF. 90033.
SOURCE: VIROLOGY, (1992) 190 (2), 849-855.
CODEN: VIRLAX. ISSN: 0042-6822.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB In efforts to elucidate the proximal leukemogens that might be produced during a feline leukemia virus (FeLV) infection of cats, homologous **recombinations** between molecularly cloned exogenous and endogenous FeLV proviruses of known sequences were examined in **cell cultures** in vitro. A plasmid containing an infectious member of

the most commonly occurring FeLV subgroup (FeLV subgroup A or FeLV-A) was coexpressed with noninfectious constructs containing the envelope (env) gene of an endogenously inherited FeLV-like feline genomic element in transfected feline fibroblasts. The viruses generated were selected for their ability to propagate in human cells which are resistant to infection by the parental ectropic FeLV-A or the noninfectious endogenous constructs. An analysis of the recombinants thus derived identified a limited number of sites in the env gene which were preferentially utilized in the generation of recombinant FeLVs under the selection conditions used. These sites were clustered in the surface glycoprotein (SU) moiety of the env gene, and it appeared that most, but not all, of the US gene product of FeLV-A, beginning from the N-terminus, can be replaced by sequences from an endogenous element, still allowing the virus to be biologically viable. In fact, these substitutions in the env gene expanded infectivity of the parental FeLV-A from ecotropic to polytropic cell tropism. Additionally, substitutions in the SU region yielded many recombinants in which a primary neutralizing **pentapeptide** epitope of FeLV-A was altered because of its variance in the endogenous element. In several of the recombinants, this sequence was also found to be frequently mutated. Consistent with the changes identified in this antibody-binding domain, the recombinant viruses were only weakly inhibited by a monoclonal antibody directed against this epitope, while FeLV-A was highly sensitive to neutralization.

L5 ANSWER 4 OF 4 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 92307057 EMBASE
DOCUMENT NUMBER: 1992307057
TITLE: Biologically selected recombinants between feline leukemia virus (FeLV) subgroup A and an endogenous FeLV element.
AUTHOR: Sheets R.L.; Pandey R.; Klement V.; Grant C.K.; Roy-Burman P.
CORPORATE SOURCE: Department of Pathology, S. California Univ. Sch. of Medicine,Los Angeles, CA 90033, United States
SOURCE: Virology, (1992) 190/2 (849-855).
ISSN: 0042-6822 CODEN: VIRLAX
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English
AB In efforts to elucidate the proximal leukemogens that might be produced during a feline leukemia virus (FeLV) infection of cats, homologous **recombinations** between molecularly cloned exogenous and endogenous FeLV proviruses of known sequences were examined in **cell cultures** in vitro. A plasmid containing an infectious member of the most commonly occurring FeLV subgroup (FeLV subgroup A or FeLV-A) was coexpressed with noninfectious constructs containing the envelope (env) gene of an endogenously inherited FeLV-like feline genomic element in transfected feline fibroblasts. The viruses generated were selected for their ability to propagate in human cells which are resistant to infection by the parental ecotropic FeLV-A or the noninfectious endogenous constructs. An analysis of the recombinants thus derived identified a limited number of sites in the env gene which were preferentially utilized in the generation of recombinant FeLVs under the selection conditions used. These sites were clustered in the surface glycoprotein (SU) moiety of the env gene, and it appeared that most, but not all, of the SU gene product of FeLV-A, beginning from the N-terminus, can be replaced by sequences from an endogenous element, still allowing the virus to be biologically viable. In fact, these substitutions in the env gene expanded infectivity of the parental FeLV-A from ecotropic to polytropic cell tropism. Additionally, substitutions in the SU region yielded many recombinants in which a primary neutralizing **pentapeptide**

epitope of FeLV-A was altered because of its variance in the endogenous element. In several of the recombinants, this sequence was also found to be frequently mutated. Consistent with the changes identified in this antibody-binding domain, the recombinant viruses were only weakly inhibited by a monoclonal antibody directed against this epitope, while FeLV-A was highly sensitive to neutralization.

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=> s s l2 and l5 and combinatorial p library
MISSING OPERATOR S L2
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s l2 and l5 and combinatorial p library
L6            0 L2 AND L5 AND COMBINATORIAL P LIBRARY

=> s l2 and l5
L7            4 L2 AND L5

=> s l7 and librar
=> s l7 and combinatorial with library
L8            0 L7 AND COMBINATORIAL WITH LIBRARY

=> s l7 and screening
L9            0 L7 AND SCREENING

=> s l2 and library
L10         467 L2 AND LIBRARY

=> s l10 and combinatorial
L11         115 L10 AND COMBINATORIAL

=> s l11 and inhibition with peptides
L12           0 L11 AND INHIBITION WITH PEPTIDES

=> s l11 and enhancing(n)peptide
L13           0 L11 AND ENHANCING(N) PEPTIDE

=>  s l11 and inhibition(n)peptides
L14           0 L11 AND INHIBITION(N) PEPTIDES

=> s l11 and inhibition (n) peptides
L15           0 L11 AND INHIBITION (N) PEPTIDES

=>  s l11 and concatemer
=> s l11 and concatemers
L16           0 L11 AND CONCATEMERS

=> s l11m with concatamers
L17           0 L11M WITH CONCATAMERS

=> s end

SEARCH ENDED BY USER

=> s

ENTER LOGIC EXPRESSION, QUERY NAME, OR (END):

ENTER LOGIC EXPRESSION, QUERY NAME, OR (END):log h
   1 FILES SEARCHED...
L18        1097 LOG H
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=> s l11 with concatamer
MISSING OPERATOR L11 WITH
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s l11(w)concatamer
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L61(W)CONCATAMER'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L62(W)CONCATAMER'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L63(W)CONCATAMER'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L64(W)CONCATAMER'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L65(W)CONCATAMER'
L19 0 L11(W) CONCATAMER

=> d l11 1-10 ibib abs

L11 ANSWER 1 OF 115 MEDLINE
ACCESSION NUMBER: 2000495123 MEDLINE
DOCUMENT NUMBER: 20389530 PubMed ID: 10931191
TITLE: Highly potent inhibitors of human cathepsin L identified by screening **combinatorial pentapeptide** amide collections.
AUTHOR: Brinker A; Weber E; Stoll D; Voigt J; Muller A; Sewald N; Jung G; Wiesmuller K H; Bohley P
CORPORATE SOURCE: Physiologisch-chemisches Institut and Naturwissenschaftliches und Medizinisches an der Universitat Tubingen, Germany.
SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (2000 Aug) 267 (16) 5085-92.
Journal code: EMZ; 0107600. ISSN: 0014-2956.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20001027
Last Updated on STN: 20001027
Entered Medline: 20001018

AB By screening a **combinatorial pentapeptide** amide collection in an inhibition assay, we systematically evaluated the potential of 19 proteinogenic amino acids and seven nonproteinogenic amino acids to serve as building blocks for inhibitors of human cathepsin L. Particularly efficient were aromatic, bulky, hydrophobic amino-acid residues, especially leucine, and positively charged residues, especially arginine. Building blocks for potential inhibitory peptides were combined by random selection from their activity pattern. This random approach for the design of inhibitors was introduced to compensate for the inaccuracy induced by shifted docking of **combinatorial** compound collections at the active center of cathepsin L. Thereby, we obtained structurally defined **pentapeptide** amides which inhibited human cathepsin L at nanomolar concentrations. Among the most potent novel inhibitors, one peptide, RKLLW-NH2, shares the amphiphilic character of the nonamer fragment VMNGLQNRK of the autoinhibitory, substrate-like, but reverse-binding prosegment of human cathepsin L which blocks the active center of the enzyme. Obviously, RKLLW-NH2 carries the functions that are important for enzyme-peptide interaction in a condensed form. This hypothesis was confirmed by structure-activity studies using truncated and

modified **pentapeptides**.

L11 ANSWER 2 OF 115 MEDLINE
ACCESSION NUMBER: 2000241347 MEDLINE
DOCUMENT NUMBER: 20241347 PubMed ID: 10780435
TITLE: DNA binding affinity of **pentapeptides** selected from **combinatorial library**.
AUTHOR: Alam M R; Maeda M; Sasaki S
CORPORATE SOURCE: Graduate School of Pharmaceutical Sciences, Kyushu University, Fukuoka, Japan.
SOURCE: NUCLEIC ACIDS SYMPOSIUM SERIES, (1999) (42) 173-4.
Journal code: O8N; 8007206. ISSN: 0261-3166.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200006
ENTRY DATE: Entered STN: 20000706
Last Updated on STN: 20000706
Entered Medline: 20000629

AB The **combinatorial** method has been applied to determine peptide ligands to the duplex DNA by using the solid-state **pentapeptide library** and the target-DNA conjugated magnetic beads. Seventy-one sequences were determined as ligands for AT duplex. Interestingly, hydrophobic amino acids such as Phe, Ile and Gly were most frequently determined. Relative binding affinity of the selected **pentapeptides** with the various DNA sequences was estimated by ethidium displacement assay in 10 mM SHE buffer. FQGII constituted of amino acids that were most frequently determined in the random screening showed highest binding affinity to the duplex DNA.

L11 ANSWER 3 OF 115 MEDLINE
ACCESSION NUMBER: 2000187600 MEDLINE
DOCUMENT NUMBER: 20187600 PubMed ID: 10722724
TITLE: Substrate specificity and inhibition studies of human serotonin N-acetyltransferase.
COMMENT: Erratum in: J Biol Chem 2000 Dec 15;275(50):39799
AUTHOR: Ferry G; Loynel A; Kucharczyk N; Bertin S; Rodriguez M; Delagrange P; Galizzi J P; Jacoby E; Volland J P; Lesieur D; Renard P; Canet E; Fauchere J L; Boutin J A
CORPORATE SOURCE: Division de Pharmacologie Moleculaire et Cellulaire, Institut de Recherches Servier, 125 Chemin de Ronde, 78290 Croissy sur Seine, France.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Mar 24) 275 (12) 8794-805.
Journal code: HIV; 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000505
Last Updated on STN: 20010702
Entered Medline: 20000427

AB Arylalkylamine N-acetyltransferase (AANAT) catalyzes the reaction of serotonin with acetyl-CoA to form N-acetylserotonin and plays a major role in the regulation of the melatonin circadian rhythm in vertebrates. In the present study, the human cloned enzyme has been expressed in bacteria, purified, cleaved, and characterized. The specificity of the human enzyme toward substrates (natural as well as synthetic arylethylamines) and cosubstrates (essentially acyl homologs of acetyl-CoA) has been investigated. Peptide **combinatorial libraries** of tri-,

tetra-, and **pentapeptides** with various amino acid compositions were also screened as potential sources of inhibitors. We report the findings of several peptides with low micromolar inhibitory potency. For activity measurement as well as for specificity studies, an original and rapid method of analysis was developed. The assay was based on the separation and detection of N-[(3)H]acetylarylethylamine formed from various arylethylamines and tritiated acetyl-CoA, by means of high performance liquid chromatography with radiochemical detection. The assay proved to be robust and flexible, could accommodate the use of numerous synthetic substrates, and was successfully used throughout this study. We also screened a large number of pharmacological bioamines among which only one, tranylcypromine, behaved as a substrate. The synthesis and survey of simple arylethylamines also showed that AANAT has a large recognition pattern, including compounds as different as phenyl-, naphthyl-, benzothienyl-, or benzofuranyl-ethylamine derivatives. An extensive enzymatic study allowed us to pinpoint the amino acid residue of the **pentapeptide** inhibitor, S 34461, which interacts with the cosubstrate-binding site area, in agreement with an in silico study based on the available coordinates of the hAANAT crystal.

L11 ANSWER 4 OF 115 MEDLINE
ACCESSION NUMBER: 2000185245 MEDLINE
DOCUMENT NUMBER: 20185245 PubMed ID: 10722170
TITLE: DNA-binding peptides searched from the solid-phase **combinatorial library** with the use of the magnetic beads attaching the target duplex DNA.
AUTHOR: Alam M R; Maeda M; Sasaki S
CORPORATE SOURCE: Graduate School of Pharmaceutical Sciences, Kyushu University, Fukuoka, Japan.
SOURCE: BIOORGANIC AND MEDICINAL CHEMISTRY, (2000 Feb) 8 (2) 465-73.
Journal code: B38; 9413298. ISSN: 0968-0896.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000421
Last Updated on STN: 20000421
Entered Medline: 20000411

AB We have exhibited successful and rapid screening of DNA-binding peptide ligands from solid-phase **library** beads with the use of the target DNA-conjugated magnetic beads. The target duplex DNA (3) has a polyether linker between two complementary sequences (T4A3G-ether linker-CT3A4) and is stable in the duplex form during the selection procedure. Finally, 71 **pentapeptide** sequences were identified from the solid-phase **pentapeptide library**. From an analysis of the peptide sequences identified in this study, it has been revealed that peptide ligands contain hydrophobic amino acids as the major component. The synthetic peptides with identified sequences and a combination of the major components have exhibited moderate to high binding affinity to the duplex DNA in competition experiments with ethidium-DNA complexes.

L11 ANSWER 5 OF 115 MEDLINE
ACCESSION NUMBER: 2000166989 MEDLINE
DOCUMENT NUMBER: 20166989 PubMed ID: 10700472
TITLE: Minimal peptide length requirements for CD4(+) T cell clones--implications for molecular mimicry and T cell survival.
AUTHOR: Hemmer B; Kondo T; Gran B; Pinilla C; Cortese I; Pascal J; Tzou A; McFarland H F; Houghten R; Martin R

CORPORATE SOURCE: Cellular Immunology Section, Neuroimmunology Branch, NINDS, National Institutes of Health, Building 10, Room 5B-16, 10 Center Drive, MSC 1400, Bethesda, MD 20892, USA.
SOURCE: INTERNATIONAL IMMUNOLOGY, (2000 Mar) 12 (3) 375-83. Journal code: AY5; 8916182. ISSN: 0953-8178.
PUB. COUNTRY: ENGLAND: United Kingdom Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 20000512 Last Updated on STN: 20000512 Entered Medline: 20000501

AB CD4(+) T lymphocytes usually recognize peptides of 12-16 amino acids in the context of HLA class II molecules. We have recently used synthetic peptide **combinatorial libraries** to dissect in detail antigen recognition by autoreactive CD4(+) T cell clones (TCC). The results of these studies demonstrated that antigen recognition by T cells is highly degenerate and that many cross-reactive ligands can be defined, some of which much more potent than the selecting autoantigen. Based on these observations, we examined the response of a myelin basic protein-specific HLA class II-restricted CD4(+) TCC to truncation variants of optimal ligands. Surprisingly, **pentapeptides**, tetrapeptides and even tripeptides derived from different segments of the optimal ligands were recognized by the TCC, and some were even more potent than the selecting autoantigen. In addition, these peptides enhanced the survival of the TCC at low concentration. The relevance of this finding was supported by the generation of **pentapeptide**-specific CD4(+) TCC from peripheral blood lymphocytes. These observations not only change existing views on the length requirements for activation of CD4(+) HLA class II-restricted T cells, but also extend our knowledge about the flexibility of TCR recognition and the potential for cross-reactivity in the immune system.

L11 ANSWER 6 OF 115 MEDLINE
ACCESSION NUMBER: 1999221187 MEDLINE
DOCUMENT NUMBER: 99221187 PubMed ID: 10206346
TITLE: Investigation of S-farnesyl transferase substrate specificity with **combinatorial** tetrapeptide **libraries**.
AUTHOR: Boutin J A; Marande W; Petit L; Loynel A; Desmet C; Canet E; Fauchere J L
CORPORATE SOURCE: Department of Peptides and Combinatorial Chemistry, Institut de Recherches SERVIER, Suresnes, France.. jaboutin@servier.fr
SOURCE: CELLULAR SIGNALLING, (1999 Jan) 11 (1) 59-69. Journal code: AVB; 8904683. ISSN: 0898-6568.
PUB. COUNTRY: ENGLAND: United Kingdom Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990614 Last Updated on STN: 19990614 Entered Medline: 19990528

AB Using biased tetrapeptide **libraries** made up of proteinogenic amino acids of the general formula Cys-O2-X3-X4, we searched for new substrates of partly purified rat brain S-farnesyl transferase (FTase). To achieve this task, an assay was developed in which the consumption of the co-substrate (farnesyl pyrophosphate) was measured. After three steps of deconvolution including each synthesis and enzymatic assay, the most efficient substrates found under these particular conditions were

Cys-Lys-Gln-Gln (peptide I) and Cys-Lys-Gln-Met (peptide II). As a control, we used another tetrapeptide **library** (Cys-Val-O3-X4) in which the valine position was arbitrarily fixed, corresponding to Cys-Val-Ile-Met in the CAAX box of K-RasB, although this sublibrary was only marginally active compared with Cys-Lys-X3-X4 in the first round of deconvolution. The best substrate sublibrary was Cys-Val-Thr-X4, threonine being more favourable than the aliphatic amino acids (Val, Ile, Leu, Ala) in this position. Deconvolution finally led to Cys-Val-Thr-Gln, -Met, -Thr and -Ser as the most efficient substrates of FTase. Those tetrapeptides were not substrates of a partly purified geranylgeranyl transferase 1 (GGTase1). We also investigated the influence of the -1 position (at the N-terminus of cysteine) on the specificity of the enzyme, by using a series of **pentapeptides** constructed on the basis of the best tetrapeptide core (peptide 1). Among this family of analogues, only His-Cys-Lys-Gln-Gln did not behave as a substrate, whereas all the other **pentapeptides** were measurable substrates, with Gly-, Asn- and Thr-Cys-Lys-Gln-Gln displaying kinetic constants similar to that of Cys-Lys-Gln-Gln. The present work provides strong evidence that the best tetrapeptide substrates of FTase do not necessarily belong to the classical CAAX box, in which A's are lipophilic residues, but rather contain hydrophilic amino acids in the middle of their sequences. Among them, peptides I and II are potent FTase in vitro substrates that are not recognised by GGTase1 and might be new starting points for the design of FTase inhibitors.

L11 ANSWER 7 OF 115 MEDLINE
ACCESSION NUMBER: 1999155049 MEDLINE
DOCUMENT NUMBER: 99155049 PubMed ID: 10037445
TITLE: N-domain selectivity of angiotensin I-converting enzyme as assessed by structure-function studies of its highly selective substrate, N-acetyl-seryl-aspartyl-lysyl-proline.
AUTHOR: Michaud A; Chauvet M T; Corvol P
CORPORATE SOURCE: Institut National de la Sante et de la Recherche Medicale, Unite 36, College de France, Paris.
SOURCE: BIOCHEMICAL PHARMACOLOGY, (1999 Mar 15) 57 (6) 611-8. Journal code: 9Z4; 0101032. ISSN: 0006-2952.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990316
Last Updated on STN: 19990316
Entered Medline: 19990304

AB The physiological functions of angiotensin I-converting enzyme (ACE) are not limited to its cardiovascular role. ACE constantly degrades N-acetyl-seryl-aspartyl-lysyl-proline (AcSDKP), a natural circulating regulator of the hematopoietic stem cell proliferation, and thereby may be involved in hematopoietic stem cell regulation. AcSDKP is hydrolyzed 50-fold faster by the N-domain active site compared to the C-domain active site. The aim of the present study was to investigate which aminoacid residues from AcSDKP are required to ensure N-domain specificity. Several peptides were designed by progressively increasing the length of the peptidic chain from a tripeptide to a **pentapeptide**. Kinetic studies of the wild-type ACE and of the two ACE mutants containing a single active domain (N- or C-domain) were performed using Bz (benzoyl) Asp-Lys-Pro, benzoyl-glycyl (Bz-Gly)-Asp-Lys-Pro, and Bz-Gly-Ser-Asp-Lys-Pro (with its intermediate product Bz-Gly-Ser-Asp) as substrates. The unexpected importance of an aspartic acid in the P1 position was discovered, as well as the interaction of the P2 and P3 positions in the substrate to increase or decrease N-domain specificity. Substrates longer than five residues may involve interdependence between subsites. Finally,

the discovery of highly specific and novel N-domain substrates cannot be predicted from single subsite mapping, but may require other approaches such as **combinatorial** peptide **libraries**.

L11 ANSWER 8 OF 115 MEDLINE
ACCESSION NUMBER: 1998362517 MEDLINE
DOCUMENT NUMBER: 98362517 PubMed ID: 9697191
TITLE: Focus-2D: a new approach to the design of targeted **combinatorial** chemical **libraries**.
AUTHOR: Cho S J; Zheng W; Tropsha A
CORPORATE SOURCE: Laboratory for Molecular Modeling, School of Pharmacy, University of North Carolina, Chapel Hill 27599-7360, USA.
CONTRACT NUMBER: HD03310 (NICHD)
MH 40537 (NIMH)
MH33127 (NIMH)
SOURCE: PACIFIC SYMPOSIUM ON BIOCOMPUTING, (1998) 305-16.
Journal code: CWQ; 9711271.
PUB. COUNTRY: Singapore
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199810
ENTRY DATE: Entered STN: 19990106
Last Updated on STN: 19990106
Entered Medline: 19981027

AB A strategy for rational design of targeted **combinatorial libraries** is described. The aim of this approach is to select a subset of available building blocks for the **library** synthesis that are most likely to be present in the active compounds. Building blocks that are used in the underlying **combinatorial** chemical reaction are randomly assembled to produce virtual **combinatorial library** compounds, which are represented by various chemical descriptors. Stochastic algorithms (simulated annealing, genetic algorithms, neural net methods) are used to search the potentially large structural space of virtual chemical **libraries** in order to identify compounds similar to lead compound(-s). The selection of a virtual molecule as a candidate for the targeted **library** is based either on its chemical similarity to a biologically active probe or on its biological activity predicted from a pre-constructed QSAR equation. Frequency analysis of building block composition of the selected virtual compounds identifies building blocks that can be used in **combinatorial** synthesis of chemical **libraries** with high similarity to the lead compound(-s). This method is applied to rational design of the **library** with bradykinin potentiating activity. Twenty eight bradykinin potentiating **pentapeptides** were used as a training set for the development of a QSAR equation, and, alternatively, two active **pentapeptides**, VEWAK and VKWAP, were used as probe molecules. In each case, the frequency distribution of amino acids in the top 100 peptides suggested by the method resembles the frequency distribution of amino acids found in the active peptides. The results obtained after GA optimization also compared favorably with those obtained by the exhaustive analysis of all possible 3.2 millions **pentapeptides**.

L11 ANSWER 9 OF 115 MEDLINE
ACCESSION NUMBER: 1998199336 MEDLINE
DOCUMENT NUMBER: 98199336 PubMed ID: 9538521
TITLE: Rational **combinatorial library** design.
2. Rational design of targeted **combinatorial** peptide **libraries** using chemical similarity probe and the inverse QSAR approaches.
AUTHOR: Cho S J; Zheng W; Tropsha A

CORPORATE SOURCE: Laboratory for Molecular Modeling, School of Pharmacy, University of North Carolina, Chapel Hill 27599, USA.
CONTRACT NUMBER: HD03310 (NICHD)
MH 40537 (NIMH)
MH33127 (NIMH)
SOURCE: JOURNAL OF CHEMICAL INFORMATION AND COMPUTER SCIENCES, (1998 Mar-Apr) 38 (2) 259-68.
Journal code: HNT; 7505012. ISSN: 0095-2338.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199804
ENTRY DATE: Entered STN: 19980507
Last Updated on STN: 19980507
Entered Medline: 19980428

AB We have developed a novel strategy for rational design of targeted peptide **libraries**. The goal of this method is to select a subset of natural amino acids that are most likely to be present in active peptides for the synthesis of **library**. Two different protocols are employed where chemical structures of peptides are described either by topological indices or by a combination of physicochemical descriptors for individual amino acids. The selection of a peptide as a candidate for the targeted **library** is based either on its chemical similarity to a biologically active probe or on its biological activity predicted from a preconstructed quantitative structure-activity (QSAR) equation. The optimization of the **library** is achieved by means of genetic algorithms (GA). This method was tested by rational design of the **library** with bradykinin-potentiating activity. Twenty-eight bradykinin-potentiating **pentapeptides** were used as a training set for the development of a QSAR equation, and, alternatively, two active **pentapeptides**, VEWAK and VKWAP, were used as probe molecules. In each case, the frequency distribution of amino acids in the top 100 peptides suggested by the method resembles the frequency distribution of amino acids found in the active peptides. The results obtained after GA optimization also compared favorably with those obtained by the exhaustive analysis of all possible 3.2 million **pentapeptides**.

L11 ANSWER 10 OF 115 MEDLINE
ACCESSION NUMBER: 97348576 MEDLINE
DOCUMENT NUMBER: 97348576 PubMed ID: 9204560
TITLE: Synthetic peptide **combinatorial libraries** : a method for the identification of bioactive peptides against phytopathogenic fungi.
AUTHOR: Reed J D; Edwards D L; Gonzalez C F
CORPORATE SOURCE: Department of Plant Pathology and Microbiology, Texas A&M University, College Station 77843-2132, USA.
SOURCE: MOLECULAR PLANT-MICROBE INTERACTIONS, (1997 Jul) 10 (5) 537-49.
Journal code: A9P; 9107902. ISSN: 0894-0282.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199709
ENTRY DATE: Entered STN: 19970922
Last Updated on STN: 19990129
Entered Medline: 19970909

AB Synthetic **combinatorial libraries** were evaluated with an iterative process to identify a hexapeptide with broadspectrum activity against selected phytopathogenic fungi. A D-amino acid hexapeptide (FRLKFH) and **pentapeptide** (FRLHF) exhibited activity against

Fusarium oxysporum f. sp. lycopersici, Rhizoctonia solani (anastomosis group 1), Ceratocystis fagacearum, and Pythium ultimum. The peptides showed no hemolytic or mutagenic activity. Fluorescent microscopy studies with a membrane impermeant dye indicated that fungal cytoplasmic membranes were compromised rapidly and that the nuclear membrane was also affected.

=> s l11 and inhibition
L20 18 L11 AND INHIBITION

=> d l20 1-5 ibib abs

L20 ANSWER 1 OF 18 MEDLINE
ACCESSION NUMBER: 2000495123 MEDLINE
DOCUMENT NUMBER: 20389530 PubMed ID: 10931191
TITLE: Highly potent inhibitors of human cathepsin L identified by screening **combinatorial pentapeptide** amide collections.
AUTHOR: Brinker A; Weber E; Stoll D; Voigt J; Muller A; Sewald N; Jung G; Wiesmuller K H; Bohley P
CORPORATE SOURCE: Physiologisch-chemisches Institut and Naturwissenschaftliches und Medizinisches an der Universitat Tubingen, Germany.
SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (2000 Aug) 267 (16) 5085-92.
Journal code: EMZ; 0107600. ISSN: 0014-2956.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20001027
Last Updated on STN: 20001027
Entered Medline: 20001018
AB By screening a **combinatorial pentapeptide** amide collection in an **inhibition** assay, we systematically evaluated the potential of 19 proteinogenic amino acids and seven nonproteinogenic amino acids to serve as building blocks for inhibitors of human cathepsin L. Particularly efficient were aromatic, bulky, hydrophobic amino-acid residues, especially leucine, and positively charged residues, especially arginine. Building blocks for potential inhibitory peptides were combined by random selection from their activity pattern. This random approach for the design of inhibitors was introduced to compensate for the inaccuracy induced by shifted docking of **combinatorial** compound collections at the active center of cathepsin L. Thereby, we obtained structurally defined **pentapeptide** amides which inhibited human cathepsin L at nanomolar concentrations. Among the most potent novel inhibitors, one peptide, RKLLW-NH2, shares the amphiphilic character of the nonamer fragment VMNGLQNRK of the autoinhibitory, substrate-like, but reverse-binding prosegment of human cathepsin L which blocks the active center of the enzyme. Obviously, RKLLW-NH2 carries the functions that are important for enzyme-peptide interaction in a condensed form. This hypothesis was confirmed by structure-activity studies using truncated and modified **pentapeptides**.

L20 ANSWER 2 OF 18 MEDLINE
ACCESSION NUMBER: 2000187600 MEDLINE
DOCUMENT NUMBER: 20187600 PubMed ID: 10722724
TITLE: Substrate specificity and **inhibition** studies of human serotonin N-acetyltransferase.
COMMENT: Erratum in: J Biol Chem 2000 Dec 15;275(50):39799
AUTHOR: Ferry G; Loynel A; Kucharczyk N; Bertin S; Rodriguez M;

Delagrange P; Galizzi J P; Jacoby E; Volland J P; Lesieur D; Renard P; Canet E; Fauchere J L; Boutin J A

CORPORATE SOURCE: Division de Pharmacologie Moleculaire et Cellulaire, Institut de Recherches Servier, 125 Chemin de Ronde, 78290 Croissy sur Seine, France.

SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Mar 24) 275 (12) 8794-805.
Journal code: HIV; 2985121R. ISSN: 0021-9258.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000505
Last Updated on STN: 20010702
Entered Medline: 20000427

AB Arylalkylamine N-acetyltransferase (AANAT) catalyzes the reaction of serotonin with acetyl-CoA to form N-acetylserotonin and plays a major role in the regulation of the melatonin circadian rhythm in vertebrates. In the present study, the human cloned enzyme has been expressed in bacteria, purified, cleaved, and characterized. The specificity of the human enzyme toward substrates (natural as well as synthetic arylethylamines) and cosubstrates (essentially acyl homologs of acetyl-CoA) has been investigated. Peptide **combinatorial libraries** of tri-, tetra-, and **pentapeptides** with various amino acid compositions were also screened as potential sources of inhibitors. We report the findings of several peptides with low micromolar inhibitory potency. For activity measurement as well as for specificity studies, an original and rapid method of analysis was developed. The assay was based on the separation and detection of N-[(3)H]acetylarylethylamine formed from various arylethylamines and tritiated acetyl-CoA, by means of high performance liquid chromatography with radiochemical detection. The assay proved to be robust and flexible, could accommodate the use of numerous synthetic substrates, and was successfully used throughout this study. We also screened a large number of pharmacological bioamines among which only one, tranylcypromine, behaved as a substrate. The synthesis and survey of simple arylethylamines also showed that AANAT has a large recognition pattern, including compounds as different as phenyl-, naphthyl-, benzothienyl-, or benzofuranyl-ethylamine derivatives. An extensive enzymatic study allowed us to pinpoint the amino acid residue of the **pentapeptide** inhibitor, S 34461, which interacts with the cosubstrate-binding site area, in agreement with an in silico study based on the available coordinates of the hAANAT crystal.

L20 ANSWER 3 OF 18 MEDLINE

ACCESSION NUMBER: 95195296 MEDLINE
DOCUMENT NUMBER: 95195296 PubMed ID: 7888715

TITLE: Synthesis of an N-3-guanidinopropylglycine (Narg) derivative as a versatile building block for solid-phase peptide and peptoid synthesis.

AUTHOR: Heizmann G; Felder E R

CORPORATE SOURCE: Ciba Pharmaceuticals Division, Basel, Switzerland.

SOURCE: PEPTIDE RESEARCH, (1994 Nov-Dec) 7 (6) 328-32.
Journal code: BE1; 8913494. ISSN: 1040-5704.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199504
ENTRY DATE: Entered STN: 19950427
Last Updated on STN: 19950427
Entered Medline: 19950420

AB N-(2,2,5,7,8-Pentamethylchroman-6-sulfonyl)-N'-3- (N-9-fluorenylmethoxycarbonyl-glycinyl)propylguanidine (1) was prepared and utilized as an arginine surrogate (Narg) building block compatible with solid-phase synthesis according to the Fmoc methodology. Narg is potentially useful in the assembly of **combinatorial** compound **libraries** or in the preparation of modified peptides. The applicability of this building block was demonstrated by its incorporation into an analogue of Thr-Arg-Ser-Ala-Trp, a **pentapeptide** for which **inhibition** of osteoclastic bone resorption was claimed. The modified **pentapeptide** showed an increased proteolytic stability when compared to the original inhibitor.

L20 ANSWER 4 OF 18 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:232927 CAPLUS
DOCUMENT NUMBER: 134:248736
TITLE: Highly potent inhibitors of human cathepsin L identified by screening **combinatorial pentapeptide** amide collections
AUTHOR(S): Brinker, Achim; Weber, Ekkehard; Stoll, Dieter; Voigt, Jurgen; Muller, Annett; Sewald, Norbert; Jung, Gunther; Wiesmuller, Karl-Heinz; Bohley, Peter
CORPORATE SOURCE: Physiol.-chem. Inst., Univ. Tubingen, Germany
SOURCE: European Journal of Biochemistry (2000), 267(16), 5085-5092
CODEN: EJBCAI; ISSN: 0014-2956
PUBLISHER: Blackwell Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB By screening a **combinatorial pentapeptide** amide collection in n **inhibition** assay, we systematically evaluated the potential of 19 proteinogenic amino acids and seven nonproteinogenic amino acids to serve as building blocks for inhibitors of human cathepsin L. Particularly efficient were arom., bulky, hydrophobic amino-acid residues esp. leucine, and pos. charged residues, esp. arginine. Building blocks for potential inhibitory peptides were combined by random selection from their activity pattern. This random approach for the design of inhibitors was introduced to compensate for the inaccuracy induced by shifted docking of **combinatorial** compd. collections at the active center of cathepsin L. Thereby, we obtained structurally defined **pentapeptide** amides which inhibited human cathepsin L at nanomolar concns. Among the most potent novel inhibitors, one peptide, RKLLW-NH2, shares the amphiphilic character of the nonamer fragment VMNGLQNRK of the autoinhibitory, substrate-like, but reverse-binding prosegment of human cathepsin L which blocks the active center of the enzyme. Obviously, RKLLW-NH2 carries the functions that are important for enzyme-peptide interaction in a condensed form. This hypothesis was confirmed by structure-activity studies using truncated and modified **pentapeptides**.
REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L20 ANSWER 5 OF 18 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:223526 CAPLUS
DOCUMENT NUMBER: 133:39768
TITLE: Substrate specificity and **inhibition** studies of human serotonin N-acetyltransferase
AUTHOR(S): Ferry, Gilles; Loynel, Armelle; Kucharczyk, Nathalie; Bertin, Sophie; Rodriguez, Marianne; Delagrange,